

## CLAIMS

1. A plant comprising a transgenic rootstock resistant to a viral disease other than by means of expression of an anti-viral protein and a scion susceptible to the viral disease, wherein the grafted plant is resistant to said viral disease.
- 5 2. The plant according to claim 1, wherein the transgenic rootstock resistant to a viral disease comprises a nucleic acid sequence having at least 90% identity to at least one segment of the viral genome.
- 10 3. The plant according to claim 2, wherein the transgenic rootstock resistant to a viral disease comprises a DNA construct designed for generating siRNAs targeted to the at least one segment of the viral genome.
4. The plant according to claim 2, wherein the at least one segment of the viral genome encodes a viral protein or parts thereof.
- 15 5. The plant according to claim 4, wherein the viral protein is selected from the group consisting of a viral coat protein, a viral replication protein, a viral movement protein or parts thereof.
6. The plant according to claim 5, wherein the viral protein is a viral replication protein or part thereof.
- 20 7. The plant according to claim 6, wherein the transgenic rootstock is resistant to a disease caused by a soil-borne virus.
8. The plant according to claim 7, being protected from a disease caused by a soil-borne virus selected from the group consisting of nematode-transmitted viruses: Nepoviruses: *Arabis* mosaic virus, *Grapevine* fanleaf virus, *Tomato* black ring virus, *Raspberry* ringspot virus, *Tomato* ringspot virus, and *Tobacco* ringspot virus; Tobraviruses: *Pea* early browning virus, *Tobacco* rattle virus and *Pepper* ringspot virus; fungal-transmitted viruses: *Cucumber* leafspot virus, *Cucumber* necrosis virus, *Melon* necrotic spot virus, *Red* clover necrotic mosaic virus, *Squash* necrosis virus, *Tobacco* necrosis satellite virus, *Lettuce* big-vein virus, *Pepper* yellow vein virus, *Beet* necrotic yellow vein virus, *Beet* soil-borne virus, *Oat* golden stripe virus, *Peanut* clump virus, *Potato* mop top virus, *Rice* stripe necrosis virus, *Soil-borne* wheat mosaic virus, *Barley* mild mosaic virus, *Barley* yellow mosaic virus, *Oat* mosaic virus, *Rice* necrosis
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mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad bean necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

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10 9. The plant according to claim 4, wherein the at least one segment of the viral genome encodes a putative 54 kDa protein being a fragment of the replication protein of cucumber fruit mottle mosaic virus (CFMMV).

15 10. The plant according to claim 9, wherein the at least one segment of the viral genome encoding a putative 54 kDa protein has the sequence set forth in SEQ ID NO:1.

11. The plant according to claim 10, being protected from a disease caused by a soil-borne virus of the tobamovirus genus.

12. The plant according to claim 11, being protected from a disease caused by CFMMV.

20 13. The plant according to claim 12, being of the Cucurbitaceae family.

14. The plant according to claim 13, being a cucumber plant.

25 15. The plant according to claim 3, wherein the DNA construct comprises nucleic acid sequence encoding an RNA sequence that forms at least one double-stranded RNA molecule, wherein the double stranded RNA molecule mediates cleavage of the at least one segment of the viral genome.

16. The plant according to claim 15, wherein the DNA construct comprises:

30 a. at least one plant expressible promoter operably linked to;

b. a nucleic acid sequence encoding an RNA sequence that forms at least one double stranded RNA, wherein the double stranded RNA molecule comprises a first nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the

sense nucleotide sequence of the target segment of the viral genome and a second nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the complementary sequence of the sense nucleotide sequence of said target segment of said viral genome; and optionally

5 c. a transcription termination signal.

17. The plant according to claim 16, wherein the first and the second nucleotide sequences are separated by a spacer sequence.

18. The plant according to claim 17, wherein the spacer sequence comprises a  
10 sequence of an intron.

19. The plant according to claim 18, wherein the spacer sequence comprises an intron of the castor bean catalase gene, having the sequence set forth in SEQ ID NO:3.

20. The plant according to claim 19, wherein the DNA construct comprises the  
15 first and the second nucleotide sequences operably linked to the same promoter.

21. The plant according to claim 20, being resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

20 22. The plant according to claim 21, wherein the soil-borne virus is selected from the group consisting of nematode-transmitted viruses: Nepoviruses: *Arabis* mosaic virus, *Grapevine* fanleaf virus, *Tomato* black ring virus, *Raspberry* ringspot virus, *Tomato* ringspot virus, and *Tobacco* ringspot virus; *Tobraviruses*: *Pea* early browning virus, *Tobacco* rattle virus and *Pepper* ringspot virus; fungal-transmitted viruses: *Cucumber* leafspot virus, *Cucumber* necrosis virus, *Melon* necrotic spot virus, *Red* clover necrotic mosaic virus, *Squash* necrosis virus, *Tobacco* necrosis satellite virus, *Lettuce* big-vein virus, *Pepper* yellow vein virus, *Beet* necrotic yellow vein virus, *Beet* soil-borne virus, *Oat* golden stripe virus, *Peanut* clump virus, *Potato* mop top virus, *Rice* stripe necrosis virus, *Soil-borne* wheat mosaic virus, *Barley* mild mosaic virus,  
25 *Barley* yellow mosaic virus, *Oat* mosaic virus, *Rice* necrosis mosaic virus, *Wheat* spindle streak mosaic virus and *Wheat* yellow mosaic virus; viruses  
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transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad bean necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

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23. The plant according to claim 21, wherein the virus transmitted by a vector affecting the aerial parts of the plant is of a family selected from the group consisting of: Caulimoviridae, Geminiviridae, Circoviridae, Reoviridae, Tarticiviridae, Bromoviridae, Comoviridae, Potyviridae, Tombusviridae, Sequiviridae, Clostroviridae and Luteoviridae; Tobamovirus, Tobravirus, Potexvirus, Carlavirus, Allexivirus, Capillovirus, Foveavirus, Trichovirus, Vitivirus, Furovirus, Pecluvirus, Pomovirus, Benyvirus, Hordeivirus, Sobemovirus, Marafivirus, Tymovirus, Idaeovirus, Ourmivirus, Umbravirus.
24. The plant according to claim 15, wherein the at least one segment of the viral genome comprises the 3' end of Zucchini Yellow Mosaic Virus (ZYMV) genome.
25. The plant according to claim 24, wherein the at least one segment of the viral genome comprises the nucleic acid sequence set forth in SEQ ID NO:2.
26. The plant according to claim 16, wherein the first nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the nucleotide sequence set forth in SEQ ID NO:2 and fragments thereof.
27. The plant according to claim 26, wherein the second nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the complement of the nucleotide sequence set forth in SEQ ID NO:2 and fragments thereof.
28. The plant according to claim 27, being resistant to a disease caused by a virus from the Potyviridae family.
29. The plant according to claim 28, being resistant to ZYMV.
30. The plant according to claim 2, wherein the nucleic acid sequence further comprises at least one expression control sequence, selected from the group

consisting of a promoter, an enhancer, a transcription factor, a splicing signal, and a termination sequence.

31. The plant according to claim 30, wherein the promoter is a constitutive promoter.
- 5 32. The plant according to claim 3, wherein the nucleic acid sequence further comprises a selectable marker.
33. The plant according to claim 32, wherein the selectable marker is selected from a polynucleotide sequence encoding a product conferring antibiotic resistance and a reporter gene encoding a detectable product.
- 10 34. The plant according to claim 30, wherein the transcription termination signal is the NOS terminator.
35. A method for producing a plant resistant to a viral disease comprising:
  - a. providing a transgenic rootstock resistant to the viral disease other than by means of expression of an anti-viral protein;
  - 15 b. providing a scion susceptible to said viral disease; and
  - c. grafting the scion onto the rootstock;  
as to obtain an engrafted plant resistant to said viral disease.
36. The method according to claim 35, wherein the rootstock is transformed with a nucleic acid sequence having at least 90% identity to at least one segment of the viral genome as to produce a transgenic rootstock resistant to the viral disease.
- 20 37. The method of claim 36, wherein the rootstock is transformed with a DNA construct designed for generating siRNAs targeted to the at least one segment of the viral genome.
- 25 38. The method according to claim 36, wherein the at least one segment of the viral genome encodes a viral protein or parts thereof.
39. The method according to claim 38, wherein the viral protein is selected from the group consisting of a viral coat protein, a viral replication protein, a viral movement protein or parts thereof.
- 30 40. The method according to claim 39, wherein the viral protein is a viral

replication protein or part thereof.

41. The method according to claim 40, wherein the transgenic rootstock is  
resistant to a disease caused by a soil-borne virus.
42. The method according to claim 41 wherein the plant is protected from a  
5 disease caused by a soil-borne virus selected from the group consisting of  
nematode-transmitted viruses: Nepoviruses: *Arabis* mosaic virus, *Grapevine*  
fanleaf virus, *Tomato* black ring virus, *Raspberry* ringspot virus, *Tomato*  
ringspot virus, and *Tobacco* ringspot virus; Tobraviruses: *Pea* early browning  
10 virus, *Tobacco* rattle virus and *Pepper* ringspot virus; fungal-transmitted  
viruses: *Cucumber* leafspot virus, *Cucumber* necrosis virus, *Melon* necrotic  
spot virus, *Red* clover necrotic mosaic virus, *Squash* necrosis virus, *Tobacco*  
necrosis satellite virus, *Lettuce* big-vein virus, *Pepper* yellow vein virus, *Beet*  
necrotic yellow vein virus, *Beet* soil-borne virus, *Oat* golden stripe virus,  
15 *Peanut* clump virus, *Potato* mop top virus, *Rice* stripe necrosis virus, Soil-borne  
wheat mosaic virus, *Barley* mild mosaic virus, *Barley* yellow mosaic virus, *Oat*  
mosaic virus, *Rice* necrosis mosaic virus, *Wheat* spindle streak mosaic virus  
and *Wheat* yellow mosaic virus; viruses transmitted via root wound:  
20 *Tobamovirus* genera: *Tobacco* mosaic virus, *Tomato* mosaic virus, *Cucumber*  
green mottle mosaic tobamovirus, *Cucumber* fruit mottle mosaic virus, *Kyuri*  
green mottle mosaic virus, *Odontoglossum* ringspot virus, *Paprika* mild mottle  
virus, *Pepper* mild mottle virus, *Ribgrass* mosaic virus and *Tobacco* mild green  
mosaic virus; and viruses transmitted by unknown rout: *Watercress* yellow spot  
virus, *Broad* been necrotic wilt virus, *Peach* rosette mosaic virus and *Sugarcane*  
chlorotic streak virus.
- 25 43. The method according to claim 38, wherein the transgenic rootstock  
comprises a nucleic acid sequence encoding a putative 54 kDa protein being a  
fragment of the replication protein of *cucumber* fruit mottle mosaic virus  
(CFMMV).
44. The method according to claim 43, wherein the transgenic rootstock  
30 comprises a nucleic acid sequence encoding a putative 54 kDa protein having  
the sequence set forth in SEQ ID NO:1.
45. The method according to claim 44, wherein the plant is protected from a

disease caused by a soil-borne virus of the tobamovirus genus.

46. The method according to claim 45, wherein the plant is protected from a disease caused by CFMMV.

47. The method according to claim 46, wherein the plant is of the Cucurbitaceae 5 family.

48. The method of claim 47, wherein the plant is a cucumber plant.

49. The method according to claim 37, wherein the DNA construct comprises 10 nucleic acid sequence encoding an RNA sequence that forms at least one double-stranded RNA molecule, wherein the double stranded RNA molecule mediates cleavage of the at least one segment of the viral genome.

50. The method according to claim 49 wherein the DNA construct comprises:

- a. at least one plant expressible promoter operably linked to;
- b. a nucleic acid sequence encoding an RNA sequence that forms at least one double stranded RNA, wherein the double stranded RNA molecule comprises a first nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the sense nucleotide sequence of the target segment of the viral genome and a second nucleotide sequence of at least 20 contiguous nucleotides having at least 90% sequence identity to the complementary sequence of the sense nucleotide sequence of said target segment of said viral genome; and optionally
- c. a transcription termination signal.

51. The method according to claim 50, wherein the first and the second nucleotide sequences are separated by a spacer sequence.

52. The method according to claim 51, wherein the spacer sequence comprises a 25 sequence of an intron.

53. The method according to claim 52, wherein the spacer sequence comprises an intron of the castor bean catalase gene, having the sequence set forth in SEQ ID NO:3.

54. The method according to claim 53, wherein the DNA construct comprises the 30 first and the second nucleotide sequences operably linked to the same

promoter.

55. The method according to claim 54, wherein the plant is resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

5 56. The method according to claim 65, wherein the soil-borne virus is selected from the group consisting of nematode-transmitted viruses: Nepoviruses: Arabis mosaic virus, Grapevine fanleaf virus, Tomato black ring virus, Raspberry ringspot virus, Tomato ringspot virus, and Tobacco ringspot virus; Tobraviruses: Pea early browning virus, Tobacco rattle virus and Pepper ringspot virus; fungal-transmitted viruses: Cucumber leafspot virus, Cucumber necrosis virus, Melon necrotic spot virus, Red clover necrotic mosaic virus, Squash necrosis virus, Tobacco necrosis satellite virus, Lettuce big-vein virus, Pepper yellow vein virus, Beet necrotic yellow vein virus, Beet soil-borne virus, Oat golden stripe virus, Peanut clump virus, Potato mop top virus, Rice stripe necrosis virus, Soil-borne wheat mosaic virus, Barley mild mosaic virus, Barley yellow mosaic virus, Oat mosaic virus, Rice necrosis mosaic virus, Wheat spindle streak mosaic virus and Wheat yellow mosaic virus; viruses transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad bean necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 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3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 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7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400

58. The method according to claim 49, wherein the at least one segment of the viral genome comprises the 3' end of Zucchini Yellow Mosaic Virus (ZYMV) genome.

59. The method according to claim 49, wherein the at least one segment of the viral genome comprises the nucleic acid sequence set forth in SEQ ID NO:2.

60. The method according to claim 50, wherein the first nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the nucleotide sequence set forth in SEQ ID NO:2 and fragments thereof.

61. The method according to claim 50, wherein the second nucleotide sequence comprises a nucleic acid sequence having at least 90% identity to the complement of the nucleotide sequence set forth in SEQ ID NO:2 and fragments thereof.

10 62. The method according to claim 61, wherein the plant is resistant to a disease caused by a virus from the Potyviridae family.

15 63. The method according to claim 62, wherein the plant is resistant to ZYMV.

64. An engrafted plant produced by the method of any one of claims 35-63.

65. The plant according to claim 64, being resistant to resistant to a virus selected from the group consisting of a soil-borne virus and a virus transmitted by a vector affecting the aerial part of the plant.

20 66. The plant according to claim 65, being resistant to a soil-borne virus selected from the group consisting of nematode-transmitted viruses: Nepoviruses: *Arabis mosaic virus*, *Grapevine fanleaf virus*, *Tomato black ring virus*, *Raspberry ringspot virus*, *Tomato ringspot virus*, and *Tobacco ringspot virus*; Tobraviruses: *Pea early browning virus*, *Tobacco rattle virus* and *Pepper ringspot virus*; fungal-transmitted viruses: *Cucumber leafspot virus*, *Cucumber necrosis virus*, *Melon necrotic spot virus*, *Red clover necrotic mosaic virus*, *Squash necrosis virus*, *Tobacco necrosis satellite virus*, *Lettuce big-vein virus*, *Pepper yellow vein virus*, *Beet necrotic yellow vein virus*, *Beet soil-borne virus*, *Oat golden stripe virus*, *Peanut clump virus*, *Potato mop top virus*, *Rice stripe necrosis virus*, *Soil-borne wheat mosaic virus*, *Barley mild mosaic virus*, *Barley yellow mosaic virus*, *Oat mosaic virus*, *Rice necrosis mosaic virus*, *Wheat spindle streak mosaic virus* and *Wheat yellow mosaic virus*; viruses

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transmitted via root wound: Tobamovirus genera: Tobacco mosaic virus, Tomato mosaic virus, Cucumber green mottle mosaic tobamovirus, Cucumber fruit mottle mosaic virus, Kyuri green mottle mosaic virus, Odontoglossum ringspot virus, Paprika mild mottle virus, Pepper mild mottle virus, Ribgrass mosaic virus and Tobacco mild green mosaic virus; and viruses transmitted by unknown rout: Watercress yellow spot virus, Broad bean necrotic wilt virus, Peach rosette mosaic virus and Sugarcane chlorotic streak virus.

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67. The plant according to claim 65, being resistant to a virus transmitted by a vector affecting the aerial parts of the plant of a family selected from the group consisting of: Caulimoviridae, Geminiviridae, Circoviridae, Reoviridae, Tarticiviridae, Bromoviridae, Comoviridae, Potyviridae, Tombusviridae, Sequiviridae, Clostroviridae and Luteoviridae; Tobamovirus, Tobravirus, Potexvirus, Carlavirus, Allexivirus, Capillovirus, Foveavirus, Trichovirus, Vitivirus, Furovirus, Pecluvirus, Pomovirus, Benyvirus, Hordeivirus, Sobemovirus, Marafivirus, Tymovirus, Idaeovirus, Ourmivirus, Umbravirus.